

RESULT 2
ABK92167
ID ABK92167 standard; DNA; 3810 BP.
XX
AC ABK92167;
XX
DT 15-AUG-2002 (first entry)
XX
DE 
XX
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.
XX
OS Mammalia.
XX
PN WO200230268-A2.
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PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 16-MAR-2001; 2001US-0276888P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288589P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
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DR WPI; 2002-471335/50.
DR P-PSDB; ABG61852.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
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PS Claim 22; Page 339-340; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3810
Score:	1123.00	Matches:	1123
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.6%	Indels:	0
DB:	6	Gaps:	0

US-10-643-795A-123 (1-1127) x ABK92167 (1-3810)

Qy 5 ThrGluLysProThrAspAlaTyrGlyGluLeuAspPheThrGlyAlaGlyArgLysHis 24

Db	3	ACGGAGAACCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGCCGGCGCAAGCAC	62
Qy	25	SerAsnPheLeuArgLeuSerAspArgThrAspProAlaAlaValTyrSerLeuValThr	44
Db	63	AGCAATTCCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGCTTATAGTCTGGTCACA	122
Qy	45	ArgThrTrpGlyPheArgAlaProAsnLeuValValSerValLeuGlyGlySerGlyGly	64
Db	123	CGCACATGGGGCTTCCGTGCCCGAACCTGGTGGTGTCACTGCTGGGGATCGGGGGC	182
Qy	65	ProValLeuGlnThrTrpLeuGlnAspLeuLeuArgArgGlyLeuValArgAlaAlaGln	84
Db	183	CCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCCTGGCTGGTGGGGCTGCCAG	242
Qy	85	SerThrGlyAlaTrpIleValThrGlyGlyLeuHisThrGlyIleGlyArgHisValGly	104
Db	243	AGCACAGGAGCCTGGATTGTCACTGGGGCTGCACACGGGATCGCCGGATGTTGGT	302
Qy	105	ValAlaValArgAspHisGlnMetAlaSerThrGlyGlyThrLysValValAlaMetGly	124
Db	303	GTGGCTGTACGGGACCATCAGATGGCCAGCAGTGGGGCACCAAGGTGGTGGCATGGGT	362
Qy	125	ValAlaProTrpGlyValValArgAsnArgAspThrLeuIleAsnProLysGlySerPhe	144
Db	363	GTGGCCCCCTGGGGTGTGGTCGGAAATAGAGACACCCATCATACACCCCAAGGGCTCGTTC	422
Qy	145	ProAlaArgTyrArgTrpArgGlyAspProGluAspGlyValGlnPheProLeuAspTyr	164
Db	423	CCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCAGTTCCCTGGACTAC	482
Qy	165	AsnTyrSerAlaPhePheLeuValAspAspGlyThrHisGlyCysLeuGlyGlyGluAsn	184
Db	483	AACTACTCGGCCTTCTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGCGAGAAC	542
Qy	185	ArgPheArgLeuArgLeuGluSerTyrIleSerGlnGlnLysThrGlyValGlyGlyThr	204
Db	543	CGCTTCCGCTTGCCCTGGAGTCCTACATCTCACAGCAGAACGGCGTGGAGGGACT	602
Qy	205	GlyIleAspIleProValLeuLeuLeuIleAspGlyAspGluLysMetLeuThrArg	224
Db	603	GGAATTGACATCCCTGCTCTGCTCTCTGATTGATGGTATGAGAACATGTTGACCGCA	662
Qy	225	IleGluAsnAlaThrGlnAlaGlnLeuProCysLeuLeuValAlaGlySerGlyAla	244
Db	663	ATAGAGAACGCCACCCAGGCTCAGCTCCATGTCTCTCGTGGCTGGCTCAGGGGAGCT	722
Qy	245	AlaAspCysLeuAlaGluThrLeuGluAspThrLeuAlaProGlySerGlyAlaArg	264
Db	723	CGGGACTGCCTGGCGGAGACCTTGGAAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCAGG	782
Qy	265	GlnGlyGluAlaArgAspArgIleArgArgPhePheProLysGlyAspLeuGluValLeu	284
Db	783	CAAGGCGAACGCCAGATCGAATCAGGCCTTCTTCCAAAGGGGACCTTGAGGTCTG	842
Qy	285	GlnAlaGlnValGluArgIleMetThrArgLysGluLeuLeuThrValTyrSerSerGlu	304
Db	843	CAGGCCAGGTGGAGAGGATTATGACCCGAAGGAGCTCCTGACAGTCTATTCTCTGAG	902
Qy	305	AspGlySerGluGluPheGluThrIleValLeuLysAlaLeuValLysAlaCysGlySer	324
Db	903	GATGGGTCTGAGGAATTGAGACCATAGTTGAAGGCCCTGTGAAGGCCTGTGGAGC	962
Qy	325	SerGluAlaSerAlaTyrLeuAspGluLeuArgLeuAlaValAlaTrpAsnArgValAsp	344
Db	963	TGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTGGCTGGCTTGGACCGCTGGAC	1022
Qy	345	IleAlaGlnSerGluLeuPheArgGlyAspIleGlnTrpArgSerPheHisLeuGluAla	364
Db	1023	ATTGCCAGAGTGAACCTTTCGGGGACATCCAATGGCGTCCTCCATCTGAAGCT	1082
Qy	365	SerLeuMetAspAlaLeuLeuAsnAspArgProGluPheValArgLeuLeuIleSerHis	384
Db	1083	TCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTCGTGCGCTGGCTCATTTCCAC	1142
Qy	385	GlyLeuSerLeuGlyHisPheLeuThrProMetArgLeuAlaGlnLeuTyrSerAlaAla	404

Db	1143	GGCCTCAGCCTGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGCG	1202
Qy	405	ProSerAsnSerLeuIleArgAsnLeuLeuAspGlnAlaSerHisSerAlaGlyThrLys	424
Db	1203	CCCTCCAACTCGCTCATCCGCAACCTTTGGACCAGGCGTCCCACAGCGCAGGCACCAA	1262
Qy	425	AlaProAlaLeuLysGlyGlyAlaAlaGluLeuArgProProAspValGlyHisValLeu	444
Db	1263	GCCCCAGCCCTAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGATGTGCTG	1322
Qy	445	ArgMetLeuLeuGlyLysMetCysAlaProArgTyrProSerGlyGlyAlaTrpAspPro	464
Db	1323	AGGATGCTGCTGGGAAGATGTGCGCGCGAGGTACCCCTCGGGGGCGCTGGGACCT	1382
Qy	465	HisProGlyGlnGlyPheGlyGluSerMetTyrLeuLeuSerAspLysAlaThrSerPro	484
Db	1383	CACCCAGGCCAGGGCTTCGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCG	1442
Qy	485	LeuSerLeuAspAlaGlyLeuGlyGlnAlaProTrpSerAspLeuLeuLeuTrpAlaLeu	504
Db	1443	CTCTCGTGGATGCTGGCCTCGGCAGGGCCCCCTGGAGCGACCTGCTCTTGGCACTG	1502
Qy	505	LeuLeuAsnArgAlaGlnMetAlaMetTyrPheTrpGluMetGlySerAsnAlaValSer	524
Db	1503	TTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGAGATGGGTTCCAATGCAAGTTCC	1562
Qy	525	SerAlaLeuGlyAlaCysLeuLeuLeuArgValMetAlaArgLeuGluProAspAlaGlu	544
Db	1563	TCAGCTCTGGGGCCTGTTGCTGCTCCGGGTATGGCACGCCCTGGAGCCTGACGCTGAG	1622
Qy	545	GluAlaAlaArgArgLysAspLeuAlaPheLysPheGluGlyMetGlyValAspLeuPhe	564
Db	1623	GAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTGAGGGATGGCGTTGACCTCTT	1682
Qy	565	GlyGluCysTyrArgSerSerGluValArgAlaAlaArgLeuLeuLeuArgArgCysPro	584
Db	1683	GGCGAGTGCTATCCGAGCAGTGAGGTGAGGGCTGCCGCCTCCCTCCGTCGCTGCCG	1742
Qy	585	LeuTrpGlyAspAlaThrCysLeuGlnLeuAlaMetGlnAlaAspAlaArgAlaPhePhe	604
Db	1743	CTCTGGGGGATGCCACTTGCCCTCCAGTGGCCATGCAAGCTGACGCCGTGCCCTCTT	1802
Qy	605	AlaGlnAspGlyValGlnSerLeuLeuThrGlnLysTrpTrpGlyAspMetAlaSerThr	624
Db	1803	GCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAAGTGGTGGGAGATATGCCAGCACT	1862
Qy	625	ThrProIleTrpAlaLeuValLeuAlaPhePheCysProProLeuIleTyrThrArgLeu	644
Db	1863	ACACCCATCTGGGGCCTGGTTCTCGCCTTCTTTGCCCTCCTACTCATCTACACCCGCCTC	1922
Qy	645	IleThrPheArgLysSerGluGluProThrArgGluGluLeuGluPheAspMetAsp	664
Db	1923	ATCACCTTCAGGAAATCAGAAGAGGAGCCACACGGGAGGAGCTAGAGTTGACATGGAT	1982
Qy	665	SerValIleAsnGlyGluGlyProValGlyThrAlaAspProAlaGluLysThrProLeu	684
Db	1983	AGTGTCAATTAGGGGAAGGGCCTGTCGGACGGCGGACCCAGCCGAGAAGACGCCGCTG	2042
Qy	685	GlyValProArgGlnSerGlyArgProGlyCysCysGlyGlyArgCysGlyGlyArgArg	704
Db	2043	GGGGTCCCGCGCCAGTCGGCGCTCCGGGTTGCTGCGGGGGCGCTGCGGGGGCGCCGG	2102
Qy	705	CysLeuArgArgTrpPheHisPheTrpGlyAlaProValThrIlePheMetGlyAsnVal	724
Db	2103	TGCCTACGCCGCTGGTCCACTTCTGGGCGCCGGTGACCATCTTCATGGCACAGTG	2162
Qy	725	ValSerTyrLeuLeuPheLeuLeuLeuPheSerArgValLeuLeuValAspPheGlnPro	744
Db	2163	GTCAGCTACCTGCTGTTCTTGCTGCTTTCTCGCGGGTGCTCTCGTGGATTTCAGCCG	2222
Qy	745	AlaProProGlySerLeuGluLeuLeuTyrPheTrpAlaPheThrLeuLeuCysGlu	764
Db	2223	GCGCCGCCGGCTCCCTGGAGCTGCTCTATTCTGGCTTCACGCTGCTGCGAG	2282
Qy	765	GluLeuArgGlnGlyLeuSerGlyGlyGlySerLeuAlaSerGlyGlyProGlyPro	784

Db	2283	GAAC TGCGCCAGGGCCTGAGCGAGGCAGGGCAGCCTCGCCAGCGGGGCCCGGCCT	2342
Qy	785	GlyHisAlaSerLeuSerGlnArgLeuArgLeuTyrLeuAlaAspSerTrpAsnGlnCys	804
Db	2343	GGCCATGCCTCACTGAGGCCAGCGCCTGCGCCTACCTCGCCGACAGCTGGAACCAGTGC	2402
Qy	805	AspLeuValAlaLeuThrCysPheLeuLeuGlyValGlyCysArgLeuThrProGlyLeu	824
Db	2403	GACCTAGTGGCTCTCACCTGCTTCCCTGGGGCTGGGCTGCCGGCTGACCCGGGTTG	2462
Qy	825	TyrHisLeuGlyArgThrValLeuCysIleAspPheMetValPheThrValArgLeuLeu	844
Db	2463	TACCA CCTGGGCCACTGTCCTCTGCATCGACTTCATGGTTTACCGTGCGCTGCTT	2522
Qy	845	HisIlePheThrValAsnLysGlnLeuGlyProLysIleValIleValSerLysMetMet	864
Db	2523	CACATCTTCACGGTCAACAAACAGCTGGGCCAACAGATCGTCATCGTGAGCAAGATGATG	2582
Qy	865	LysAspValPhePheLeuPhePheLeuGlyValTrpLeuValAlaTyrGlyValAla	884
Db	2583	AAGGACGTGTTCTCTCCCTCTCCCTCGGCGTGTGGCTGGTAGCCTATGGCTGGCC	2642
Qy	885	ThrGluGlyLeuLeuArgProArgAspSerAspPheProSerIleLeuArgArgValPhe	904
Db	2643	ACGGAGGGCTCCTGAGGCCACGGGACAGTGA CTTCCAACTATCCTCGGCCGCTCTC	2702
Qy	905	TyrArgProTyrLeuGlnIlePheGlyGlnIleProGlnGluAspMetAspValAlaLeu	924
Db	2703	TACCGTCCCTACCTCGAGATCTCGGGCAGATTCCCAGGAGGACATGGACGTGCCCTC	2762
Qy	925	MetGluHisSerAsnCysSerSerGluProGlyPheTrpAlaHisProProGlyAlaGln	944
Db	2763	ATGGAGCACAGCAACTGCTCGGAGCCGGCTCTGGCACACCCTCCTGGGCCAG	2822
Qy	945	AlaGlyThrCysValSerGlnTyrAlaAsnTrpLeuValValLeuLeuValIlePhe	964
Db	2823	GCGGGCACCTGCGCTCCCAGTATGCCAACTGGCTGGTGGCTGCTCCCTCGTCATCTC	2882
Qy	965	LeuLeuValAlaAsnIleLeuLeuValAsnLeuLeuIleAlaMetPheSerTyrThrPhe	984
Db	2883	CTGCTCGTGGCCAACATCCTGCTGGTCAA CTTGCTCATGCCATGTTAGTACACATT	2942
Qy	985	GlyLysValGlnGlyAsnSerAspLeuTyrTrpLysAlaGlnArgTyrArgLeuIleArg	1004
Db	2943	GGCAAAGTACAGGGCAACAGCGATCTACTGGAAAGGCGCAGCGTTACCGCCTCATCCGG	3002
Qy	1005	GluPheHisSerArgProAlaLeuAlaProProPheIleValIleSerHisLeuArgLeu	1024
Db	3003	GAATTCACCTCGGCCGCGCTGGCCCGCCCTTATCGTCATCTCCACTTGGCCCTC	3062
Qy	1025	LeuLeuArgGlnLeuCysArgArgProArgSerProGlnProSerSerProAlaLeuGlu	1044
Db	3063	CTGCTCAGGCAATTGTGCAGCGACCCGGAGCCCCAGCGCTCCCGGCCCTCGAG	3122
Qy	1045	HisPheArgValTyrLeuSerLysGluAlaGluArgLysLeuLeuThrTrpGluSerVal	1064
Db	3123	CATTTCGGGTTACCTTCTAAGGAAGCCGAGCGGAAGCTCTAACGTGGAAATCGGT	3182
Qy	1065	HisLysGluAsnPheLeuAlaArgAlaArgAspLysArgGluSerAspSerGluArg	1084
Db	3183	CATAAGGAGAACTTCTGCTGGCACCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGT	3242
Qy	1085	LeuGluArgThrSerGlnLysValAspLeuAlaLeuLysGlnLeuGlyHisIleArgGlu	1104
Db	3243	CTGGAGGCCACGTCCAGAAGCTGGACTGGCACTGAAACACCTGGACACATCCGCGAG	3302
Qy	1105	TyrGluGlnArgLeuLysValLeuGluArgGluValGlnGlnCysSerArgValLeuGly	1124
Db	3303	TACGAACAGCGCCTGAAAGTGTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCTGGGG	3362
Qy	1125	TrpValThr 1127	
Db	3363	TGGGTGACG 3371	

